Please amend the specification and claims as follows, without prejudice to subsequent renewal of the specification in its original form.

In the Specification

Please delete the paragraph at page 5, lines 16-19 and substitute therefor the following new paragraph(s):

A1

Figure 1 is a schematic representation of DNAs and PNAs. The top is a schematic of a single stranded DNA. The middle is a schematic of a single-stranded PNA. The bottom is a schematic overlay of the DNA and PNA, showing the similarity of the overall structure of the two molecules.

Please delete the paragraph at page 5, line 20-28 and substitute therefor the following new paragraph(s):

A2

Figure 2A schematically shows the use of poly-lysine for PNA-DNA hybrid detection. Figure 2B shows several histograms summarizing hybridization data for three PNAs. Figure 2C shows a histogram depicting the kinetics of PNA/DNA hybridization as detected by FP in the presence of polylysine (*see also*, Anal. Biochem. 275, 248 (1999)). Figure 2D shows several melting curves analyzed by FP. Figure 2E shows graphs depicting the effects of mismatch position on PNA/DNA duplex stability with PNA probe 188 (a 9-mer). Assay conditions were: 50 nM PNA 188, 50 mM HEPES pH 7.5, 3.3 μM Poly L-Lysine.

Please delete the paragraph at page 5, line 29 – page 6, line 7 and substitute therefor the following new paragraph(s):

A3

Figure 3A depicts a graph showing the effects of mismatch position on PNA/DNA duplex stability for PNA probe 201 (an 11-mer). Assay conditions included: 50 nM PNA 201, 50 mM HEPES pH 7.5, 3.3 μM Poly L-Lysine. Figure 3B shows graphs with the results for SNP typing in PCR products, including fluorescein labeled PNA probes. In this experiment, single stranded PCR products were 79 bases long; PNA 7637 is was a 9-mer, matching the pUC product and having a TG mismatch with the pBR product; and PNA 7699 is a 13-mer, fully complementary to both PCR products. Figure 3C shows a set of graphs showing

A3 cont.

SNP discrimination in the absence of polylysine for rhodamine labeled PNAs. Figure 3D shows melting curves for rhodamine-labeled probe 8158, including a melting curve for wild-type and G/T SNP targets, in the absence of poly-lysine.

Please delete the paragraph at page 6, lines 8-22 and substitute therefor the following new paragraph(s):

A4

Figure 4, shows additional histograms and example conclusions for the effect of polylysine on DNA/PNA duplex stability, real time detection of T7 gene 6 exonuclease degradation of a PCR product coupled with PNA probe hybridization and the effect of target size and polylysine. Figure 4A shows a graph of FP vs. temperature including the effect of poly-Lysine on PNA/DNA duplex stability. Experiments were with rhodamine labeled probes at 50mM HEPES pH7.5/ 50mM NaCl, 2μM PNA, 5μM DNA Targets, +/- 4μM pLL. Figure 4B shows histograms for rhodamine labeled PNAs, including the effect of target size and poly-lysine. Figure 4C shows real-time detection of T7 gene 6 exonuclease degradation of a PCR product coupled with PNA probe hybridization. One of the PCR strands contains four phosphorothioates at its 5' end, making it resistant to T7 gene 6 exonuclease. The enzyme hydrolyses the opposite strand to generate a single-stranded template to which the PNA probe hybridizes. The reactions were carried out in PCR buffer. The DNA targets were a 22mer (280) and 9mers (289, 290). PNA probes were 200 nM in 50 mM HEPES pH 7.5, 50 mM NaCl, with Poly-lysine at 0 or 4 μM.

Please delete the paragraph at page 6, lines 25-27 and substitute therefor the following new paragraph(s):

A5

Figure 7, Panels A-C, is a schematic illustration of a microfluidic device incorporating an external sampling pipettor as a reaction/assay receptacle in the present invention.

Please delete the paragraph at page 7, lines 4-5 and substitute therefor the following new paragraph(s):

A6

Figures 10A-B illustrate an exemplary computer system and architecture for use with the present invention.

Please delete the paragraph at page 36, lines 26-34 and substitute therefor the following new paragraph(s):

A7

Sequences of nucleic acids used for the analysis depicted in Figure 2 include: 188: Fl-O-CAA-ATA-CTC; 201: Fl-O-TCA-AAT-ACT-CC (SEQ ID NO. 1); 202: Fl-O-GTC-AAA-TAC-TCC-A (SEQ ID NO. 2) (also labeled with BODIPY-Fl); 7637: Fl-O-CCT-GTA-GCA; 7638: Fl-O-TGC-TAC-AGG; 7699: Fl-O-CAC-CAC-GAT-GCC-T (SEQ ID NO. 3); 212 5' GCTGGAGTATTTGACCT (SEQ ID NO. 4); 244 5' TTGTTGCCAATGCTACAGGCATCGT (SEQ ID NO. 5); 245 5' TTGTTGCCAATGCTGCAGGCATCGT (SEQ ID NO. 6); and 247 5' ACGATGCCTGTAGCATTGGCAACAA (SEQ ID NO. 7). Assay conditions were: 50 nM PNA 188, 50 mM HEPES pH 7.5, 3.3 μM Poly L-Lysine.

Please delete the paragraph at page 39, lines 12-17 and substitute therefor the following new paragraph(s):

A8

The disclosure of USSN 60/203,723 is incorporated by reference in its entirety for all purposes. In addition, all publications, patents, patent applications, other documents, internet citations, CD-ROM citations and other publicly accessible information listed herein are hereby incorporated by reference for all purposes, as if each individual publication, patent, patent application or other document was specifically and individually indicated to be incorporated by reference.

In accordance with 37 CFR §1.121 a marked up version of the above-amended paragraph(s) illustrating the changes introduced by the forgoing amendment(s) are provided in Appendix A.

In the Claims: